

**Figure 1**

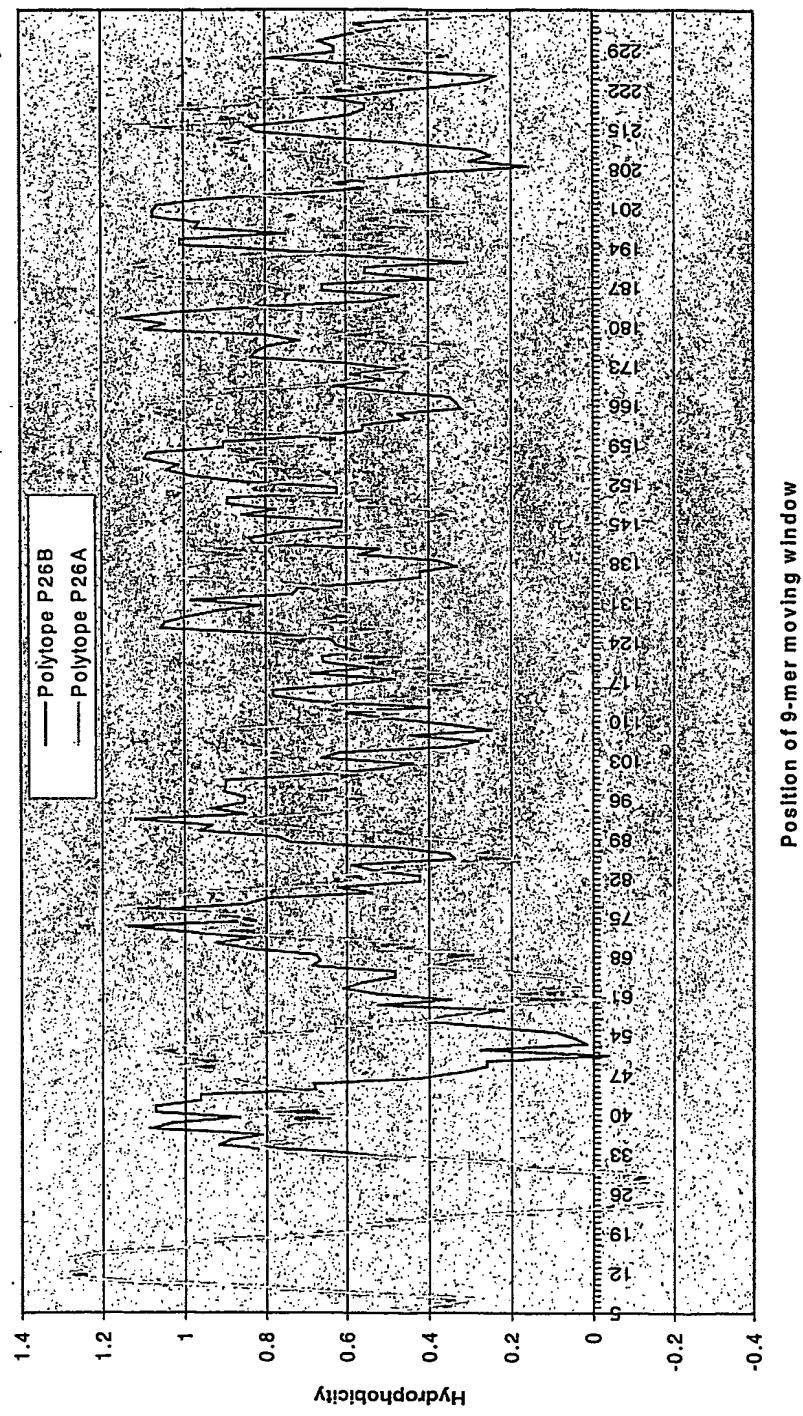
The initial three residues MVD have been introduced due to restriction sites

P26A	MVDFLRGRAYGL - PYLFWLAAI - HRCQAIRKK - RRIYDIEL - VQPPQLTLQV-GLCTLVAML - RLRAEAQVK - IEDPPFNSL - YLLEMILWRL- GGGGSTAM - AVLHHEESM - IALYLQQNWWTL-RAKFQKLL - SSSSSCPLSKI - TYGPVFMCQAKWRLQTL - RPPFIRRL - VSFIEFVGW- YPLHEQHGM - VEITPYKPTW- CLGGLLTMV - EENLLDFVRF - TYSAGIVQI - LLDFVRFMVG - EGGVGWRHW - HHHHHHHH (SEQ ID NO:94)	0.38 0.18 0.34 0.36	1.02 0.43 0.52 1.02	-0.07 0.2 0.82 -0.07	0.39 0.45 0.53 0.39	0.55 0.83 0.53 0.85	0.85 0.32 0.71 -0.06	-0.06 0.47 0.36 0.4	0.4 0.47 0.36 0.53	0.85 0.83 0.71 0.71
P26B	MVDFLRGRAYGL - PYLFWLAAI - HRCQAIRKK - RRIYDIEL - GLCTLVAML - RLRAEAQVK - IEDPPFNSL - TYSAGIVQI - LLDFVRFMGV- EGGVGWRHW - IALYLQQNWWTL - RAKFQKLL - SSSSSCPLSKI - TYGPVFMCQAKWRLQTL - RPPFIRRL - VSFIEFVGW - YPLHEQHGM- VEITPYKPTW- CLGGLLTMV - EENLLDFVRF - YIFMIWRI - GOGGSEPTAM - AVYHHEESM - YOPPOLTOV - HHHHHHHH (SEQ ID NO:95)	0.38 0.36 0.52	1.02 0.83 0.82	-0.07 0.2 0.35	0.39 0.45 0.35	0.39 0.83 0.85	0.85 0.83 0.18	-0.06 0.47 0.43	0.4 0.47 0.55	0.71 0.83 0.55

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Figure 2

## Hydrophobicity Index (Fauschere &amp; Pliska)

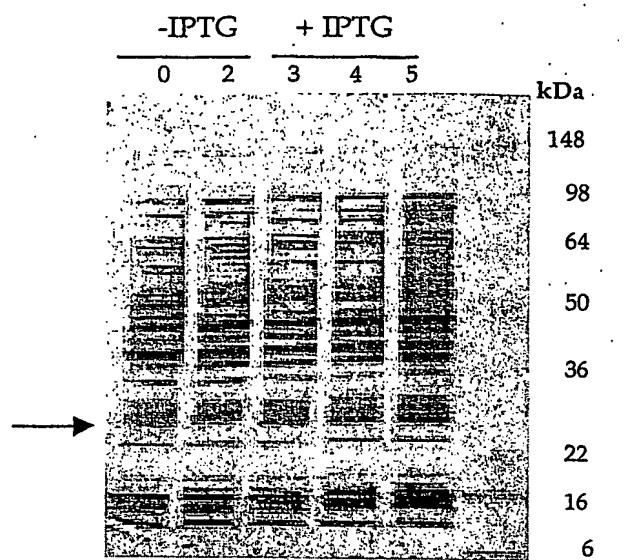
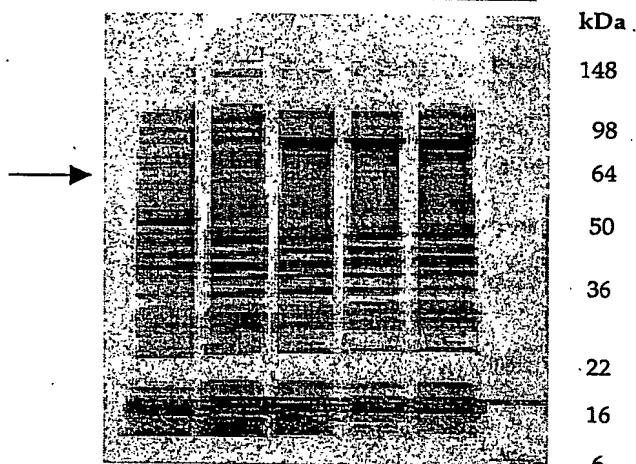


**Figure 3A** gp350/PT26A

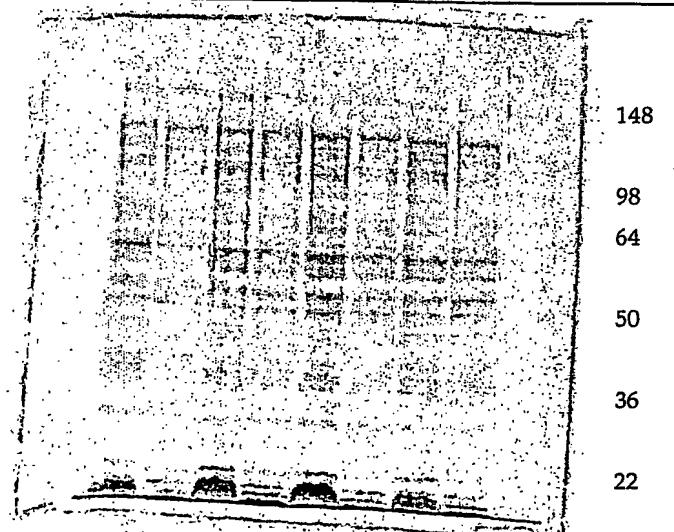
MEDPGFFNVEIPEFPFYPTCNVCTADNVNTINF DVGGKKHQLDLD**F**GQLTPHTKAVYQPRGAFGGSENAT  
 NLFLLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLI**P**E**T**V**P**  
 IKWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFN  
 T-help epitope 70  
 ITC SGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGD**C**I  
 140  
 QSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANS PNVTVTAFWAWPNNTETDFKCKWTLT  
 280  
 SGTPSGCENISGAFASNRTFDITVSGLGTAPKTLIITRTATNATTTHKVIFSKAPESTTSPTLNNTGF  
 420  
 ADPNTTGVD**F**L**R**GRAY**G**LPYLFWLA**A**I**H**RC**Q**A**I**R**K****R****I**Y**D****L****I****E****L****V****Q****P****P****Q****L****T****L****Q****V****G****L****C****T****L****V****A****M****L****R****I****R****A**  
 428 B8 A23 B27 B27 B46 A2 A3  
AQVKIEDPPFNSLYLLEM**L**WRL**G**Q**GGSPTAMAVLLHEESMIALYLOONWWTLRAKF**K**Q**LLSSC****SSCP**LSK**  
 B60 A2 B62 B35 B57/A2 B8 A11  
 ITYGPVFMC**L**QAKWRL**Q**TLR**P**PI**F**IR**R**LV**S**FI**E**FG**W**Y**P**l**H**EQ**HGM****V**E**I**TPYKPTW**C**LG**GL****L**TM**V****E****N****L**  
 A24 B8 B7 B58 B35 B44 A2  
 DFVRF**T**YSAGIV**Q****I****LLDF**VR**F**MG**V**EG**G****V**GR**W****H****HHHHHH**  
 B44 A24 A2 B44 (SEQ ID NO: 96)

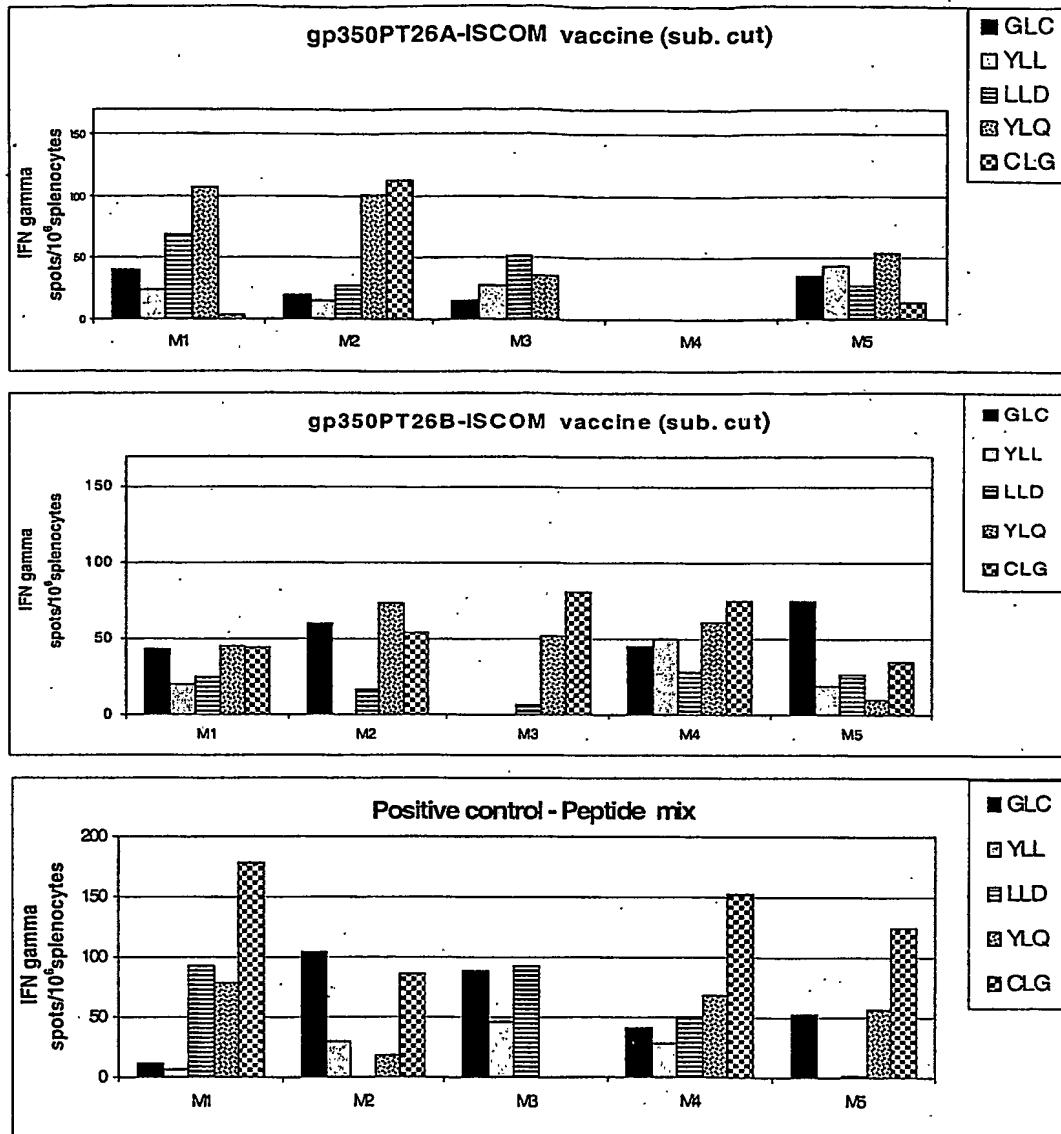
**Figure 3B** gp350/PT26B

MEDPGFFNVEIPEFPFYPTCNVCTADNVNTINF DVGGKKHQLDLD**F**GQLTPHTKAVYQPRGAFGGSENAT  
 NLFLLELLGAGELALTMRSKKLPIINVTTGEEQQVSLESVDVYFQDVFGTMWCHHAEMQNPVYLI**P**E**T**V**P**  
 IKWDNCNSTNITAVVRAQGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQVLPGDNKFN  
 T-help epitope 70  
 ITC SGYESHVPSGGILTSTSPVATPIPGTGYAYSLRLTPRPVSRFLGNNSILYVFYSGNGPKASGGD**C**I  
 140  
 QSNIVFSDEIPASQDMPTNTTDITYVGDNATYSVPMVTSEDANS PNVTVTAFWAWPNNTETDFKCKWTLT  
 280  
 SGTPSGCENISGAFASNRTFDITVSGLGTAPKTLIITRTATNATTTHKVIFSKAPESTTSPTLNNTGF  
 420  
 ADPNTTGVD**F**L**R**GRAY**G**LPYLFWLA**A**I**H**RC**Q**A**I**R**K****R****I**Y**D****L****I****E****L****V****Q****P****P****Q****L****T****L****Q****V****G****L****C****T****L****V****A****M****L****R****A****E****A****Q** VKIEDPPF  
 428 B8 A23 B27 B27 A2 A3 B60  
 NSLTYSAGIV**Q****I****LLDF**VR**F**MG**V**EG**G****V**GR**W****H****I****A****L****Y****LO****Q****N****WW****T****L****R****A****K****F****K****Q****LLSSC****SSCP**LSKITYGPVFMC  
 A24 A2 B44 B57/A2 B8 A11 A24  
 LOAKWRL**Q****T****L****R****P****P****I****F****I****R****R****L****V****S****F****I****E****F****V****G****W****Y****P****l****H**EQ**HGM****V****E****I**TPYKPTW**C**LG**GL****L**TM**V****E****N****L****LD**FR**F****Y****L****E**  
 B8 B7 B58 B35 B44 A2 B44  
 MLWRL**G**Q**GGSPTAMAVLLHEESM**V**Q****P****P****Q****L****T****L****Q****V****HHHHHH** (SEQ ID NO: 97)  
 A2 B62 B35 B46

**Figure 4A****Figure 4B****Figure 4C**

ON	hr	3 hr	1 hr	M	kDa
I	U	I	U	I	U



**Figure 5**

**Figure 6**

WO 2004/007556

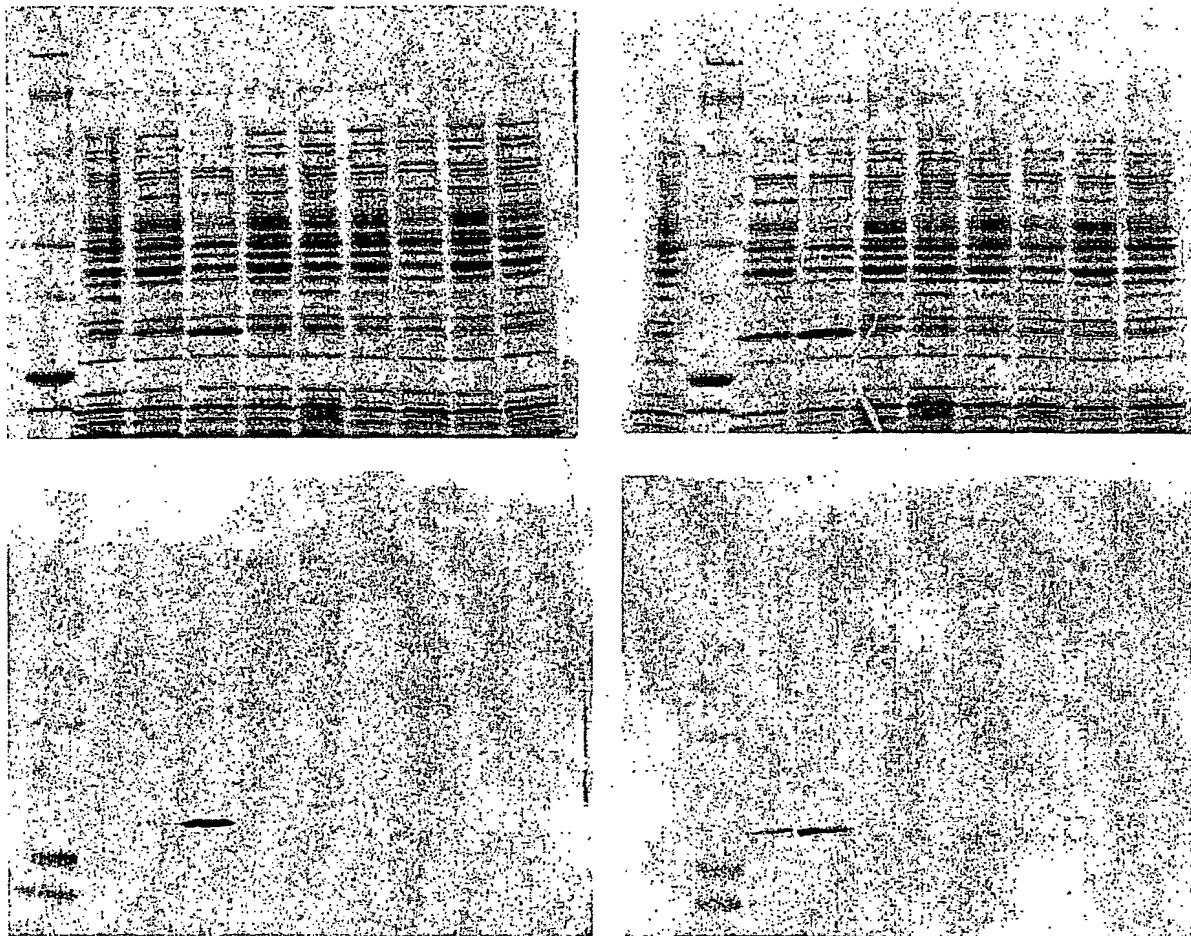
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Figure 7

**Figure 8**

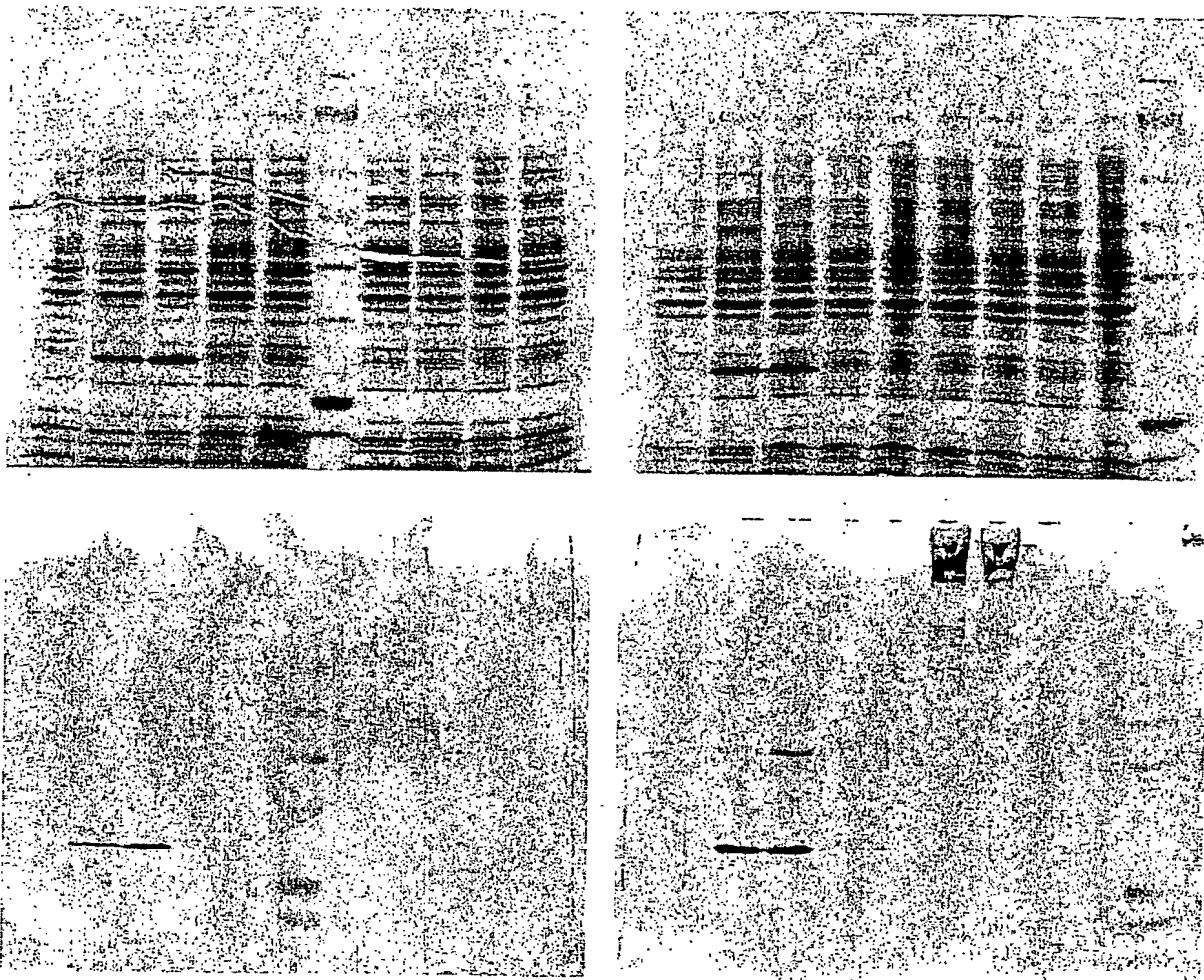
		HI values (n=3): 1.25 1.21 1.44 1.3 1.22 1.44 1.48 1.41 1.59 1.63 1.61 1.62 1.63 1.62 1.62 1.58 1.59 1.61 1.60 1.66 1.69 1.69 1.72 1.15									
		HI values (n=3): 1.46 1.68 1.55 1.44 1.61 1.67 2.24 2.07 1.93 0.73 0.10 0.38 1.35 2.36 2.19 1.87 1.65 1.41 1.88 1.77 1.58 1.17 1.23 1.59 1.22									
		YLVAYQATV - RLIVFPDLGV - TLGFAYMSK - IPFYGKAI - VLYGGVLA - CTCGSSDLV - HHHHHH (SEQ ID NO:101)									
		YLVTRHADV - WMNRLLAFA - CTCGSSDLV - HHHHHH (SEQ ID NO:102)									
HCVa	0.94	-0.3	0.61	0.9	-0.07	0.47	0.82	0.15	0.51	0.75	
0.33	0.55	0.73	0.34	0.56	0.72	0.34	0.56	0.68	0.68	0.35	
0.58	0.67	0.41	0.61	0.67	0.67	0.44	0.04				
0.47	-0.3	-0.07	0.75	0.67	0.94	0.58	0.35	0.72	0.72	0.34	
0.82	0.61	0.15	0.41	0.67	0.67	0.51	0.04				
0.82	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10	
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	
0.82	1.55	1.44	1.61	1.67	2.24	2.07	1.93	0.73	0.10		
0.47	1.46	1.68									

**Figure 9**



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Figure 10



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